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From: Pak, Yong  
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dear stic,

please find the following:

Purification and characterization of a (R)-2,3-butanediol  
dehydrogenase from *Saccharomyces cerevisiae*.

AU Heidl J; Tressl R

CS Technische Universität Berlin, Fachbereich Lebensmitteltechnologie und  
Biotechnologie.

SO ARCHIVES OF MICROBIOLOGY, (1990) 154 (3) 267-73.

Journal code: 0410427. ISSN: 0302-8933.

Molecular characterization of the *Pseudomonas putida* 2,3-butanediol  
catabolic pathway.

AU Huang M; Oppermann F B; Steinbuchel A

CS Department of Biology, Sichuan Normal University, Chengdu, China.

SO FEMS MICROBIOLOGY LETTERS, (1994 Dec 1) 124 (2) 141-50.

Journal code: 7705721. ISSN: 0378-1097.

thank you.

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## Molecular characterization of the *Pseudomonas putida* 2,3-butanediol catabolic pathway

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**Abstract:** The 2,3-butanediol dehydrogenase and the acetoin-cleaving system were simultaneously induced in *Pseudomonas putida* PpG2 during growth on 2,3-butanediol and on acetoin. Hybridization with a DNA probe covering the genes for the E1 subunits of the *Alcaligenes eutrophus* acetoin cleaving system and nucleotide sequence analysis identified *acoA* (975 bp), *acoB* (1020 bp), *acoC* (1110 bp), *acoX* (1053 bp) and *adh* (1086 bp) in a 6.3-kb genomic region. The amino acid sequences deduced from *acoA*, *acoB*, and *acoC* for E1 $\alpha$  ( $M_r$  34639), E1 $\beta$  ( $M_r$  37268), and E2 ( $M_r$  39613) of the *P. putida* acetoin cleaving system exhibited striking similarities to those of the corresponding components of the *A. eutrophus* acetoin cleaving system and of the acetoin dehydrogenase enzyme system of *Pelobacter carbinolicus* and other bacteria. Strong sequence similarities of the *adh* translational product (2,3-butanediol dehydrogenase,  $M_r$  38361) were obtained to various alcohol dehydrogenases belonging to the zinc- and NAD(P)-dependent long-chain (group I) alcohol dehydrogenases. Expression of the *P. putida* ADH in *Escherichia coli* was demonstrated. The *aco* genes and *adh* constitute presumably one single operon which encodes all enzymes required for the conversion of 2,3-butanediol to central metabolites.

**Key words:** 2,3-Butanediol dehydrogenase; Acetoin-cleaving system; Acetoin dehydrogenase enzyme system; *Pseudomonas putida*; *Alcaligenes eutrophus*; *Pelobacter carbinolicus*

### Introduction

The key reaction of the fermentative breakdown of acetoin (3-hydroxy-2-butanone) in the strictly anaerobic bacteria *Pelobacter carbinolicus* and *Clostridium magnum* is the thiamine PP<sub>1</sub> (TPP)-, coenzyme A-, and NAD-dependent cleav-

age of acetoin into acetaldehyde and acetyl coenzyme A, which is catalysed by the acetoin dehydrogenase enzyme system [1–3]. Utilization of the reduced acetoin-derivative 2,3-butanediol requires in addition 2,3-butanediol dehydrogenase which feeds the substrate to the acetoin dehydrogenase enzyme system. The structural genes of the acetoin dehydrogenase enzyme system *acoA* (encoding the  $\alpha$  subunit of the TPP-dependent acetoin dehydrogenase, E1 $\alpha$ ), *acoB* (encoding E1 $\beta$ ), *acoC* (encoding dihydrolipoamide acetyltransferase, E2), and *acoL* (encoding dihydrolipoamide dehydrogenase, E3) from both *P.*

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*carbinolicus* and *C. magnum* were found to be clustered in co-linear orientation in the genome [2,3]. In addition to the structural genes of the acetoin dehydrogenase enzyme system, *acoS* (encoding the *P. carbinolicus* lipoate synthase), *acoX* (encoding a *C. magnum* protein of unknown function), and *acoR* (encoding a putative regulatory protein) were localized within the gene cluster of the respective bacterium. A similar organization was recently also reported for the genes encoding the acetoin catabolic system of *Klebsiella pneumoniae* [4].

From the great variety of strictly respiratory acetoin-degrading bacteria, as yet only the molecular genetics of the acetoin catabolism of *Alcaligenes eutrophus* have been examined in detail [5]. The gene products and the molecular organization of the *A. eutrophus* *aco* operon (*acoXABC*) encoding the *A. eutrophus* acetoin cleaving system resemble in some aspects those of the acetoin dehydrogenase enzyme system of the anaerobic bacteria mentioned above. In contrast to the latter, *acoL* is absent in the *aco* locus of *A. eutrophus*, and the participation of a dihydro-lipoamide dehydrogenase (E3) in the acetoin cleaving system remained obscure [6]. *Pseudomonas putida*, which in contrast to *A. eutrophus*, can also use 2,3-butanediol as sole carbon source in addition to acetoin [7], is unique since this bacterium possesses three different dihydro-lipoamide dehydrogenases, of which the function of the third isoenzyme (LPD-3) is unknown [8]. As LPD-3 exhibited significant similarities to both E3 components of the acetoin dehydrogenase enzyme systems of *P. carbinolicus* [2] and *C. magnum* [3], this bacterium was chosen to investigate its acetoin-catabolic system with particular consideration to the participation of an E3 component.

## Materials and Methods

### Bacteria and media

*Pseudomonas putida* PpG2 (ATCC 23287, wild-type, kindly provided by J.R. Sokatch) and *Escherichia coli* XL1-Blue (Stratagene, La Jolla, CA) were used in this study. *P. putida* was grown

at 30°C, in mineral salts medium [9], supplemented with 0.2% (w/v) of 2,3-butanediol, acetoin, glucose or acetate as carbon source. *E. coli* was grown at 37°C in Luria-Bertani (LB) [10] medium. For enzymatic analysis the soluble cell fractions were used from cells, harvested in the late exponential growth phase, resuspended in 50 mM 2-(*N*-morpholino)propane sulfonic acid (pH 7.2), disrupted by ultrasonication, and centrifuged 50 min at 100 000 × *g*.

### Isolation and manipulation of DNA

Total genomic DNA from *P. putida* was obtained as described [11]. Plasmid DNA was isolated from *E. coli* by using the alkaline lysis method [10]. Other DNA manipulations were essentially as described [10]. To construct partial libraries, genomic DNA of *P. putida* was digested with *EcoRI*, *ApaI* or *ClaI*. DNA fragments of desired length were recovered from 0.8% (w/v) agarose gels by using a Gene Clean kit (Bio 101, La Jolla, CA) and ligated with linearized vector pBluescript KS<sup>-</sup> (Stratagene, La Jolla, CA) to transform competent cells of *E. coli* [10]. Transformants were screened by using in situ hybridization [10] with a heterologous biotinylated DNA probe. DNA sequencing was done by the dideoxy-chain termination method [12] with alkaline denatured double-stranded plasmid DNA using a T7 polymerase sequencing kit (Pharmacia LKB Biotechnology, Uppsala, Sweden). Sequence data were analysed with the Genetic Computer Group (GCG) sequence analysis software package [13].

### Assay and analysis of proteins

Activities of the enzyme components E1, E2, and E3 of the acetoin dehydrogenase enzyme system, and of 2,3-butanediol dehydrogenase were determined photometrically according to Oppermann et al. [1] and Steinbüchel and Schlegel [9], respectively. Protein was determined as described by Lowry et al. [14]. Proteins of cell extracts were separated by denaturing SDS-polyacrylamide gel electrophoresis [15]. Activity staining for E1 was done as described before [1].

Table 1  
Expressi  
Strain

<i>P. putid</i>
<i>P. putid</i>
<i>P. putid</i>
<i>E. coli</i>
<i>E. coli</i>
<i>P. puti</i>
were c
or 1.0'



Table 2

Similarities of the amino acid (aa) sequences deduced from the *P. putida* PpG2 *aco* genes to the respective *aco* gene products of *A. eutrophus* [5], *P. carbinolicus* [2], *K. pneumoniae* [4] and *C. magnum* [3]

Aa sequence deduced from <i>P. putida</i> gene	Percentage of amino acid identity to the respective <i>aco</i> gene product from			
	<i>A. eutrophus</i>	<i>P. carbinolicus</i>	<i>K. pneumoniae</i>	<i>C. magnum</i>
<i>acoA</i>	63.6	64.2	59.1	48.9
<i>acoB</i>	63.2	52.7	51.6	41.3
<i>acoC</i>	47.5	29.4	25.9	21.4
<i>acoX</i>	42.4	Not present	Not present	30.8

Values were calculated for complete sequence overlap by the program GAP [13].

## Results and Discussion

### Induction of the 2,3-butanediol-catabolic enzymes

To investigate the presence of the components of the acetoin dehydrogenase enzyme system after growth on 2,3-butanediol and on acetoin, cells of *P. putida* were grown on different substrates and assayed for their respective enzyme activities. Growth on acetoin and on 2,3-butanediol was fairly effective with doubling times ( $t_d$ ) of 2.2 h and 2.4 h, respectively, whereas on the non-acetoinogenic substrates, glucose and acetate,  $t_d$  values were obtained of 2.2 and 2.3 h, respectively. TPP-dependent acetoin dehydrogenase (E1) was only detected in the soluble cell fractions after growth on acetoin (0.070 U (mg protein)<sup>-1</sup>) or on 2,3-butanediol (0.072 U mg<sup>-1</sup>), whereas no activity was measurable after growth on either glucose or acetate. In accordance with that, one protein band with an  $R_f$ -value of 0.12 occurred during activity staining for E1 in the two protein patterns from acetoin- or 2,3-butanediol-grown cells, whereas none occurred with proteins derived from glucose- or acetate-grown cells. Expression of 2,3-butanediol dehydrogenase exhibited a similar regulatory pattern (Table 1). In

contrast, dihydrolipoamide acetyltransferase (E2) and dihydrolipoamide dehydrogenase (E3) were measured after growth on either substrate (U mg<sup>-1</sup> after growth on acetoin: E2, 0.15, E3, 0.083; 2,3-butanediol: E2, 0.15, E3, 0.064; glucose: E2, 0.30, E3, 0.085; acetate: E2, 0.21, E3, 0.23), which can be explained by the presence of the isoenzymes for E2 and E3 from the pyruvate and/or 2-oxoglutarate dehydrogenase complex. This indicated a close regulatory linkage between the expression of the *P. putida* acetoin catabolic system and 2,3-butanediol dehydrogenase which is different from the situation previously found in *A. eutrophus* [16]: although a multifunctional alcohol dehydrogenase able to oxidize 2,3-butanediol [9] is encoded in the *A. eutrophus* genome, the wild-type cannot grow on 2,3-butanediol, since this fermentative enzyme is only expressed under conditions of restricted oxygen supply.

### Identification and characterization of the structural genes encoding the acetoin cleaving system

Southern hybridization analysis of totally digested *P. putida* PpG2 genomic DNA with fragment ES25, which covered the structural genes *acoA* and *acoB* encoding E1 $\alpha$  and E1 $\beta$ , respec-

Fig. 2. Nucleotide sequence of the *P. putida* PpG2 *aco* gene cluster. Amino acids deduced from the nucleotide sequence are specified by standard one-letter abbreviations. The position of a putative -24/-12 promotor and of putative ribosomal binding sites (S/D) are indicated. The position of a putative stem-loop structure is marked by inverted arrows. Conserved amino acid residues of the putative TPP-binding region of the deduced *acoA* gene product, and conserved glycine residues flanking the putative lipoylation site of the *acoC* gene product are marked by the symbol #; the position of the lysine in the deduced *acoC* gene product, which is presumably lipoylated, is indicated by the symbol \*. The nucleotide and amino acid sequences have been submitted to the Genome Sequence Database at the Los Alamos National Laboratory under accession no. L35343.



S/D M S Q

F S D A L E D L Y I P D A A K I E A A V R K V I E A A R S A A \*

3101 GTTCTCCGACGCCCTGGAGACCTGTACATCCCTGACCGCGGGAAGATCGAGGCTGCCGTGCGCAAGGTGATCGAAGTGAAGGAGTCCCGCATGAGCC

acoC ->

I H T L T M P K W G L S M T E G R V D A W L K Q E G D E I N K G D

3201 AGATCCATACCTGACCATGCCCAAGTGGGGCCTTTTCGATGACCGAGGGCGGGTGGAGCCTGGCTCAAGCAGGAAGGCGAGAAATCAACAAGGCGA

lipoylation site

E V L D V E T D K I S S S V E A P F S G V L R R Q V A K P D E T L

3301 CGAGGTGCTGGACGTCGAGACCGACAAGATCAGCAGCAGCGTCGAAGCCCGCTTCAGTGGTGTATTGCGCCGCCAGGTGGCCAAACCGGATGAACCTTG

P V G A L L A V V V E G E A E E S E I D A V V Q R F Q A E F V A E G

3401 CCGGTGGCGCGCTGCTGGCGGTGGTGGTGAAGGCGAAGCGAGGAATCGAGATCGATCGAGTGTACAGCGCTTCAGGCGGAGTTCGTGCGCGAAG

G A D Q A Q G P A P Q K A E V G G R L L R W F E L G G E G G T P L

3501 GGGCGCGCAGCAGGCAAGGGCGGCGCGCAGAAAGCTGAAGTGGCGCGCGCTGTTCGCTGGTTCGAATGGCGGAGAAGCGGTACGCGCT

V L V H G F G G D L N N W L F N H P A L A A E R R V I A L D L P G

3601 GGTACTGGTACAGGCTTTGGCGGCGACTCAACAATGGCTGTTCACCAACCGCGCTGGCGCGGAGCGCGGATGCGCCCTGACCTGCGCGGG

H G E S A K A L Q R G D L D E L S E T V L A L L D H L D I A K A H L

3701 CACGGCGAGTGGCCAAAGGCGCTGCAACGGGCGGCGCTGGATGAAGTGAAGCGAAACCGCTGCGCCCTGCTGACACACCTGGACATCGCCAAAGGCGCAC

A G H S M G G A V S L N V A G L A P Q R V A S L S L I A S A G L G

3801 TGGCGGACACTTCATGGGGGCGCGGTGAGCTGAAGCTGGCGCGCTGGCGCGGAGCGCGGATGCGCCCTGAGCTGCGCGGATGCGCGCTGGG

E A I N G Q Y L Q G F V A A A N R N A L K P Q M V Q L F A D P A L

3901 TGAGGCAATCAATGGCGAGTACCTGCAAGGCTTTGTGGCGCGCGGAGCGCGCGCTTCACCAACCGGAGATGGTGGAGCTGTTCGCGACCGCGCACTG

V T R O M L E D M L K F K R L E G V D E A L R Q L A L A I D G R D R

4001 GTACCCGCGAGATGCTGAAGACATGCTCAAGTTCAAGCGCTGGAAGGTGTCGATGAGGCGCTTGGCGCAGTGGCATGAGCATGCGCAGCGTGACA

Q R H D L R S V L G Q H P A L V V W G G K D A I I P A S H A R K G

4101 GGCAGCGCACGACCTGCGCAGCGTGTGGCGGCGAGTCCGCGCATGGTGGTGGGGTGGCAAGGAGCGGATATCCCGCGCAGCGCACGCAAGGAAGG

P E A E V L V L P E A G H M V Q M E A A E Q V N Q Q M L A F L R K

4201 CCGCGAGCGCAAGTGTGCTGCTGCCAGGCTGGGCGATATGTCGATGAGGCGCGCGCAAGGTCAACAGCAATGCTGCAATTCCTGCGCAAG

H \* S/D M N D L S H T H M R A A V W H G R N D I R V

4301 CACTAAGCCCTTCCCGTGGAGCTGGAGAACAAATGAATGACCTGAGCCACACCCACATGCGCGCGCGCTGTGATGCGCGTAAATGATATTCGCGT

adh ->

E Q V P L P A D P A P G W V Q I K V D W C G I C G S D L H E Y V A

4401 CGAAGGTCGCCCTGCCAGCGGACCGCGCGCTGGGTGAGTCAAGTGGAGTGGTGGCGCATCTGCGGCTGCGACCTGCAAGTACGCTGCGG

G P V F I P V E A P H P L T G I Q G Q C I L G H E F C G Q I A K L G

4501 GGCCTGGTGTTCATCCCGTGGAGGACACACCGCTGACCGGCTATCCAGGCGGAGTGTCTGCGCCAGCAATTTTGGCGGAGATGCGCAAGCTTG

E G V E G F A V G D P V A A D A C Q H C G T C Y Y C T H G L Y N I

4601 GCGAAGCGGTGAGGCTTTGCGGTAGTGACCGGTGGCGCGGAGCGCTGCGCAGCATGTGTACTTGTATTACTGACCCAGCGGCTGTACAACAT

C E R L A F T G L M N N G A F A E L V N V P A N L L Y R L P Q G F

4701 CTGGAGCGCTGGCGTTTACCAGCTGATGAACAATGGCGCTTTGCGAGTGTGTCACGTACCGCGCAACCTGCGGCTTGGCGCAAGGTTTC

P P E A G A L I E P L A V G M H A V K K A G S L L G Q T V V V V G A

4801 CCGCCAGAGGCGCGGCGCTGATCGAAGCGTGGCGGTGGTATGACCGGTTGAAAGGCGCGGAGCGCTGCTTGGCGAGACCTTGTGGTGGTGGT

G T I G L C T I M C A K A A G A A Q V I A L E M S S A R K A K A K

4901 CCGGACCATCGCTGTCGACCATATGTCGCGCAAGGCTGCGGCGCGGCGCAAGTGTGCTGGAATGTCCTGCGCGCGGAGCGCAAGGCGCA

E V G A T V V L D P S Q C D A L A Q I R A L T F G L G A D V S F E

5001 AGAGGTAGCGCCACCGTGTGTCGAGGCGGCGGCTGGCGCAATCCCGCAGTACCTTTGGTGGTGGGCGGATGTGAGCTTTGAG

C I G N K H T A K L A I D T I R K A G K C V L V G I F E E P S E F N

5101 TGATCGGCAACAAGCACAGCGCAAGTGGCATGACACCATCGCAAGCGGTAAGTGGTGGTGGTATTTTGAAGGCTAGCGAGTTCA

F F E L V S T E K Q V L G A L A Y N G E F A D V I A F I A D G R L

5201 ACTTCTCGAATGTGATCCACCGAGAAGCAGTACTGGGAGCTTTGGCGTACAACCGCGAGTTTGGCGATGTGATTGCTTCAATGCTGACGCGGAGCT

D I R P L V T G R I G L E Q I V E L G F E E L V N N K E E N V K I

5301 GGATATTGCGCGCTGTGACCGCGCGGCTGGGTGGAGCAGATTGTCGAATGGGCTTCGAGGAATGGTGAACAACAAGGAGGAGACGTGAAGATC

I V S P G V R \*

5401 ATCGTTTCCCGGCTGTGCTGATTAAACCTCAAAGGCTGCGCAGATCTGTAGGAGCGGCTTGTGTGCGAAAGGGTGGCAGCGCCCAAGGG

5501 ATCTGTGATCAGGTAATATGCGGGGCGCGTTCGCGGCTTTTCGCGACAAAGGCGCTCTACACAGGTGATGCGCCAGCATCTGCCCTCGCT

5601 GTCTCAGGATCCCATTTCTGCTATACCTGCGCAGACCTATTGCGCGGTCTTCCCATGCGTCCACTGCTCCCATCACCTTGGCTTGTGCTGCGCGCC

5701 TGTGGCATGGCGAATCGCTTCCCGCGGACGACGCTTGCCTGACGCGCGGCGTTACCGGGGAGGTGGTGTGATGGCTGCTGACGGGCGAGGGCC

5801 GTATCGACTACCCCAAGCGAGCTGTGACGCGGCGCTTCAAGGACGCGAGTGGCAGCGGAGGAGAAATGGCAGCGGAGAGCGGAGGTGTACCG

5901 TGGCAGTTGCGCGGGGCTGTTCCAGGAGTGGGCGACCTGACACGCGGCGGCGCTTACCGCGGAGCTTCAAGCATGCGCGCGGATGCGGAA

6001 GGCACGCTCAAGCAAGCGACGACCTACCTGCGGAGTTCAAGGACGACCTTACGACGCGCGGCGGAACTGGAAGTGGCGGAGCGGAGCGCTACC

6101 AGGGCTGTTCGCAAGGCGAAACCAACGCGCGCGGCTACGACGAGTGCAGCGGTAACAGTTCAGTGGCGGCTTGTCAACGGCGAGCTGCAAGG

6201 CAGCGGACCTACGACGCGTGTAGCGGTGAGCAGTACATCGCGGAGTTCAAGGACAAACGCGCTGGAAGGTGCGCGCGCTTACGAAACCGCGATGCGGAT

6301 GTGTGGATTGGCGAATTC

Fig. 2 (continued).

tively,  
[5], re  
kb E

tively, of the *A. eutrophus* acetoin cleaving system [5], revealed clear signals corresponding to a 5.1-kb *EcoRI*, a 2.8-kb *ApaI* and a 3.9-kb *ClaI*

fragment. In situ hybridization with the corresponding partial libraries in *E. coli* identified four *EcoRI*, five *ApaI* and two *ClaI* clones. Se-

M S Q  
CATGAGCC  
accC ->  
K G D  
AAGGCCA

T L  
AACCCTG  
A E G  
GCCGAG  
P L  
CGCCGCT  
P G  
GCCGGGG  
A H L  
GCCACC  
L G  
TCTGGG  
A L  
TACTG  
D R  
TGTACA  
K G  
GAAGGG  
R K  
CGCAAG  
R V  
TCGCT

V A  
GTCCGC  
L G  
AGCTTG  
N I  
CAACAT  
G F  
GGTTTC  
G A  
TGGGT  
A K  
GCCAA  
E  
TTGAG  
F N  
GTTCA  
R L  
AGGCT  
I  
AGATC  
AAGGG

TCGCT  
CGGCC  
GGGCC  
TACCG  
TGAAG  
TACC  
AAGG  
TGGAT

```

1 MNDLSHTMRAAVWHGRNDLRVEDVPLPADPAPGWVQKVDWCGICGSDLHEVAGPVFI ADH P. putida
1 THTVPQNMKAAMVMTREIKIETLEVPDINHDE-LLIKVMAVGICGSDLHYTNGRI-- SoDH B. subtilis
1 MKALSCLKAEEGIMWTDVVPPELGHNDLLIKIRKTAICGTDVHIL- ThDH E. coli
1 MKAAVITKDHTEVVKDTKRLPKYGE-ALLEMEYCGVCHTDLH--VKGDF-- ADH1 Z. mobilis
1 MKAAV I LIK GICG DLH Y G CONSENSUS

61 PVEAPHPLTGIQGGCITLGEFCQOTAKIGEGVEGFAVGDPVAAD-ACOHGCTCYCTHGL ADH P. putida
57 -----GNVVEKPFILGHECAGETAAVGSSVDQKVGDRVAVE-PGVTOGRCEACKGR SoDH B. subtilis
46 -NWDEWSQRTIPVPMVVGHEVYGVVIGQEVKGIKIDRVSGE-GHITOGHCRNCRGR ThDH E. coli
48 -----GDETGRITGHEGIGIVKQVGEVTSLKAGDRASVAVWFFKCGCHCTCVSGN ADH1 Z. mobilis
I GHE G G Y FK GDRV CG C C G CONSENSUS

120 YNLCERLAFGLMN-NGAPAEELVNVNPNLLYRLPOGFPPPE-AGALIEFLAVGMHAYKKAG ADH P. putida
110 YNLCPDVQFLATPPVDGAFVQYIKMRQDFVFLIPDSLSYE-EAALIEFVSIGIHAARTK SoDH B. subtilis
105 THLCRN-TIGVGNRPGCEAEVLVIPAFAFNAKIDPNISDDL-AAIFDFGNAVHTALSFD ThDH E. coli
100 ETLGRNVE-NAGYTVDGAMAEICIVADYSVKVPDGLDPAVASSITCAGVTYKAVKVSQ ADH1 Z. mobilis
LC GAFAE A PD A P H CONSENSUS

-----NAD-binding pocket-----
178 SLGQTVVVGAGTIGLCTIMCAKAGAAVIALEMSSARKAKAKVGGATVLDSEQDA ADH P. putida
169 LQPGSTIAIMGMPVGLMAVAAKAFAGTIDVTDLEPLRLAAAKMGATHIINIREQDA SoDH B. subtilis
162 -EVGEDVLVSGAGPIGIMAAAVAKHVGARNVITDVNEYRLRLARKMGITRAVNVAKENL ThDH E. coli
159 IQPGWLAIYGLGGLGNLALQYAKNVFNKVIATDVNDEQLAFKELGADMVINEKNEDE ADH1 Z. mobilis
G G G G A AK GA VI D RL AK GAT N DA CONSENSUS

238 LAQIRALTFLGLGADVSFCIGNKHTAKLAIDTIRKAGKCVLVGL-FEEPSE--FNFFELV ADH P. putida
229 LEEIKTITNDRGVVDVAVETAGNPAALQSLASVVRGGKLAIVGLPSQNEIP--LVVPFIA SoDH B. subtilis
221 NDVMAELGMEGFDVGLMSGAPPAPRTMLDTMNHGGRIAMLGIPPSDMSIDWTKVIFKG ThDH E. coli
219 AKIQEKVGGAHATVV--TAVAKSAFNSAVEAIRAGGRVAVGLPPEKMDLSIPRLVLDG ADH1 Z. mobilis
I G DV E G A A R GG VG P CONSENSUS

295 STEKQVL-GALAYNGEFADVIAEIAIDGRLDIRPLVTGRIGLEQIVELGFEELVNNKEENV ADH P. putida
287 DNEIDYI-GIFRYANTYPKGIEFLASGIVDTKHLVTDQYSLEQTD-AMERALQFKNECL SoDH B. subtilis
281 LFIKGIY-GREMFETWYKMAA--LIQSGDLSEIITHRFSIDDFQK-GEDAMRSQSGSKV ThDH E. coli
277 IEVLGSEVGTREDRLKAFQFAEGKVKPKVTKRVEEINQIFDEMEHCKFTGRMVVDFTH ADH1 Z. mobilis
G D VT G CONSENSUS

```

Identity to ADH P. putida (%)

354	KIIVSEGVR	ADH P. putida	100
345	KVMVYENR	SoDH B. subtilis	34.5
339	ILSWD	ThDH E. coli	26.0
337	H	ADH1 Z. mobilis	30.5
		CONSENSUS	

Fig. 3. Homology of the *P. putida* PpG2 *adh* gene product to other alcohol dehydrogenases. The deduced amino acid sequence of the *P. putida* *adh* gene product was compared with the polypeptides stored in the SWISSPROT data library by using the program FASTA [13]. Microbial amino acid sequences, which gave the best sequence overlaps with the *P. putida* protein, were aligned by using the program MULTALIGN [13]. Amino acids are specified by standard one-letter abbreviations, and the numbers indicate the position of the respective residue within the protein. Regions with identity to the *P. putida* *adh* gene product shown in the upper line are shaded. Amino acids, which are present in at least three of the four proteins, are labelled as CONSENSUS; amino acids, which are conserved in all four sequences, are written in bold; the strictly conserved residues of microbial group I alcohol dehydrogenases [19] are underlined. The putative ligands of the catalytic zinc [Zn(cat)] and of the structural zinc atom [Zn(str)] as well as the putative cofactor-binding site of the *P. putida* protein are indicated above the aligned sequences. Calculation of the percentages of identity of the amino acid sequences to the *P. putida* polypeptide was done for a complete sequence overlap with the program GAP [13]. Amino acid sequences from the proteins of *B. subtilis*, *E. coli* and *Z. mobilis* were fetched from the SWISSPROT data library: SoDH, sorbitol dehydrogenase (accession no. Q06004); ThDH, threonine dehydrogenase (accession no. P07913); ADH1, alcohol dehydrogenase I (accession no. P20368).

quence analysis of the corresponding fragments (E51, A28, and C39 in Fig. 1) revealed 6318 bp of the *P. putida* genome exhibiting a G + C content of 65.1 mol%, which corresponded to the G + C content of 62.5 mol% of the genome [7]. Among 32 open reading frames (ORFs) with a minimum length of 150 bp, five (ORF1, ORF2, ORF3, ORF4, and ORF5 in Fig. 1) were identified as structural genes according to the following characteristics: (i) agreement with the *P. putida* codon preference; (ii) presence of reliable Shine/Dalgarno sequences; (iii) similarity to gene products stored in data libraries.

Due to clear homologies to the corresponding enzyme components of the acetoin catabolic systems of *A. eutrophus*, *P. carbinolicus*, *C. magnum*, and *K. pneumoniae*, ORF1 and ORF2 were identified as genes *acoA* and *acoB*, encoding the  $\alpha$  and  $\beta$  subunit of the acetoin dehydrogenase (E1), whereas ORF4 corresponded to *acoC* encoding the E2 component (Fig. 1, Table 2). A TPP-binding motif [17] was identified in the translational product of *acoA* (Fig. 2). In the translational product of *acoC*, the consensus sequence of a lipoyl-binding site [18] was localized (Fig. 2). ORF3, which was located upstream of *acoA*, exhibited strong homologies to both *acoX* translational products (Table 2), which were previously identified in the *aco* gene clusters of *C. magnum* [3] and of *A. eutrophus* [5], and was therefore referred to as *acoX*. As no further significant similarity to any other gene product was obtained, and as no clear evidence for the presence of catalytic or structural motifs was obtained from the consensus sequence of the *acoX* gene products, the function of *acoX* in the acetoin catabolism of *A. eutrophus*, *C. magnum* and *P. putida* is obscure. Closely upstream of *acoX* a motif was located which matched the enterobacterial  $\sigma^{54}$  promoter consensus sequence [5] (Fig. 2). The program STEMLOOP [13] predicted a region of dyad symmetry downstream of ORF5 (Fig. 2), suggesting that there is a possible mRNA structure with a free energy of stem-loop formation of 53.6 kJ which might serve as a transcriptional terminator. The nucleotide sequence data provided no evidence for the presence of a structural gene encoding a dihydrolipoamide dehydro-

genase, which is similar to the situation previously reported for *A. eutrophus* [5]. Thus, the participation of an E3 component in the acetoin cleaving system of strictly respiratory bacteria remains obscure.

#### Identification and characterization of *adh* encoding 2,3-butanediol dehydrogenase

Downstream of and co-linear to *acoC*, ORF5 was identified encoding a 362-amino acid polypeptide which exhibited a high degree of homology to various alcohol dehydrogenases (ADHs) belonging to the NAD(P)- and zinc-dependent long-chain (group I) ADHs [19]. It was therefore concluded that ORF5 represents an ADH structural gene. The alignment of the primary structure deduced from ORF5 with representative ADH sequences matched all 14 strictly conserved residues of microbial group I ADHs [19] including the motifs around two of the three catalytic zinc ligands (Cys<sub>46</sub> and His<sub>79</sub>) at the N-terminal part, and the NAD-binding pocket at the central part of the polypeptide (Fig. 3). In addition, the binding motif for a second zinc was identified (Cys<sub>109</sub> to Cys<sub>123</sub>), which is known to bind the non-catalytic or structural zinc in most group I ADHs [19]. Interestingly, the putative third ligand of the catalytic zinc in *P. putida* ADH was found to be a negatively charged residue (Glu<sub>165</sub>) which is also present in ADHs catalysing the oxidation of secondary alcohols (e.g. sorbitol dehydrogenase from *Bacillus subtilis*, threonine dehydrogenase from *E. coli*; Fig. 3). In almost all other ADHs, which preferentially accept primary alcohols, this position is occupied by a cysteine residue (e.g. alcohol dehydrogenase I from *Zymomonas mobilis*; Fig. 3). These sequence data correspond with a catabolic function of the *P. putida adh* gene product in feeding 2,3-butanediol to the acetoin cleaving system. In addition, the absence of promoter-like structures upstream of *adh*, *acoC*, *acoB*, and *acoA*, the presence of a reliable promoter region upstream of *acoX*, the concomitant synthesis of the acetoin-cleaving system and of the 2,3-butanediol dehydrogenase during growth on 2,3-butanediol and on acetoin provided evidence that *adh* belongs to the same operon as the four *aco* genes.

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### Heterologous expression of ADH in *E. coli*

Since fragment EA24 harbours the entire *adh* gene (Fig. 1), it was chosen for expression of ADH in *E. coli*. Crude cell extracts of IPTG-induced *E. coli* (pKS::EA24) exhibited significant 2,3-butanediol dehydrogenase activity (Table 1). No enzyme activity was detected in cells grown on glucose or in cells of *E. coli* (pBluescriptKS). In SDS-polyacrylamide gels, two distinct protein bands with estimated  $M_r$  values of 38 000 and 47 000 were visible in the protein pattern of IPTG-induced cells of *E. coli* (pKS::EA24), which did not appear in glucose-repressed *E. coli* (pKS::EA24) or in *E. coli* harbouring only the vector. The protein band corresponding to the smaller protein also appeared in the protein pat-

tern of *P. putida* PpG2 grown on acetoin or 2,3-butanediol (Fig. 4), and its size corresponded to the calculated value of the *adh* gene product ( $M_r$  38 361).

### Conclusions

The data presented here provide evidence that in *P. putida* PpG2 2,3-butanediol is metabolized (i) by oxidation to acetoin, which is catalysed by the 2,3-butanediol dehydrogenase, and (ii) by subsequent oxidative cleavage of acetoin to acetaldehyde and acetyl-CoA, which is catalysed by the acetoin cleaving system (Fig. 1E). The molecular organization of the genes involved in the second step resembled that previously reported for the respiratory acetoin-degrading *A. eutrophus* [5]: the structural genes encoding the enzyme components E1 and E2 of the acetoin cleaving system were closely clustered in the order *acoA*, *acoB* and *acoC*, and they were preceded by *acoX*, encoding a gene product of unknown function. As *adh* presumably belongs to the same operon in addition to the *aco* genes, all enzymes required for the conversion of 2,3-butanediol to central metabolites are expressed from one transcriptional unit.

### Acknowledgements

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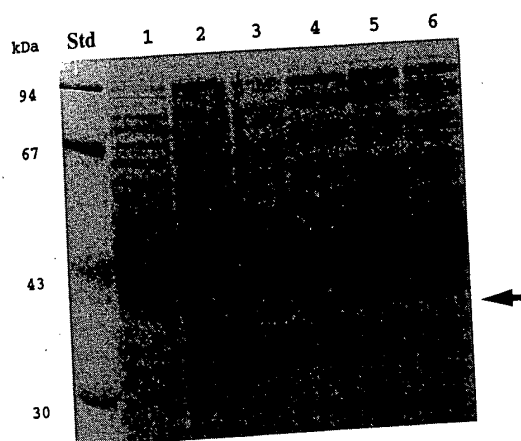


Fig. 4. Expression of *P. putida* PpG2 2,3-butanediol dehydrogenase in *E. coli*. Soluble extracts from *P. putida* PpG2 and from recombinant strains of *E. coli* XL1-Blue were obtained from cells harvested in the late exponential growth phases. Proteins were separated in an SDS-11.5% (w/v) polyacrylamide gel and stained with Serva Blue R. Molecular masses of standard proteins (lane Std) are given. The position of a protein band in lane 4 corresponding to the predicted  $M_r$  of *P. putida* 2,3-butanediol dehydrogenase is marked by an arrow. Lanes: 1, 28  $\mu$ g protein of the soluble cell fraction from *P. putida* grown on glucose; 2, 38  $\mu$ g of protein of the soluble cell fraction from *P. putida* grown on acetoin; 3, 29  $\mu$ g of protein of the soluble cell fraction from *P. putida* grown on 2,3-butanediol; 4, 25  $\mu$ g of protein of the soluble cell fraction from *E. coli* XL1-Blue(pKS::EA24) grown in the presence of 1.0 mM IPTG; 5, 28  $\mu$ g of protein of the soluble cell fraction from *E. coli* XL1-Blue(pKS::EA24) grown in the presence of 1% (w/v) glucose; 6, 31  $\mu$ g of protein of the soluble cell fraction from *E. coli* XL1-Blue(pBluescriptKS<sup>-</sup>).

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(FILE 'HOME' ENTERED AT 10:27:03 ON 06 MAY 2003)

FILE 'MEDLINE, CAPLUS, BIOSIS, AGRICOLA' ENTERED AT 10:27:08 ON 06 MAY 2003

L1 157 S BUTANEDIOL (1N) DEHYDROGENASE  
L2 3 S L1 AND PICHIA  
L3 3 DUP REM L2 (0 DUPLICATES REMOVED)  
L4 94 S L1 AND ACETOIN  
L5 9 S L1 AND (ACETOIN (2N) R)  
L6 6 DUP REM L5 (3 DUPLICATES REMOVED)

FILE 'STNGUIDE' ENTERED AT 10:29:31 ON 06 MAY 2003

FILE 'MEDLINE, CAPLUS, BIOSIS, AGRICOLA' ENTERED AT 10:33:52 ON 06 MAY 2003

L7 3 S L4 AND BUTANEDIONE  
L8 3 DUP REM L7 (0 DUPLICATES REMOVED)

FILE 'STNGUIDE' ENTERED AT 10:36:59 ON 06 MAY 2003

FILE 'MEDLINE, CAPLUS, BIOSIS, AGRICOLA' ENTERED AT 10:40:13 ON 06 MAY 2003

L9 14 S R (3N) L1  
L10 8 DUP REM L9 (6 DUPLICATES REMOVED)

FILE 'STNGUIDE' ENTERED AT 10:42:02 ON 06 MAY 2003

FILE 'MEDLINE, CAPLUS, BIOSIS, AGRICOLA' ENTERED AT 10:42:46 ON 06 MAY 2003

L11 121 S L1 AND (NAD OR NADH OR ACETOIN OR BUTANEDIONE)  
L12 66 S L1 AND (NAD OR NADH)  
L13 42 S L12 AND ACETOIN  
L14 8 S L13 AND R  
L15 5 DUP REM L14 (3 DUPLICATES REMOVED)  
L16 24 S L1 AND R  
L17 13 DUP REM L16 (11 DUPLICATES REMOVED)

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(FILE 'HOME' ENTERED AT 08:50:10 ON 08 MAY 2003)

FILE 'MEDLINE, CAPLUS, BIOSIS, AGRICOLA' ENTERED AT 08:50:16 ON 08 MAY 2003

L1 140 S ACETOIN (2N) REDUCTASE  
L2 2 S L1 AND R  
L3 1 DUP REM L2 (1 DUPLICATE REMOVED)  
L4 3 S L1 AND PICHIA  
L5 1 DUP REM L4 (2 DUPLICATES REMOVED)

FILE 'STNGUIDE' ENTERED AT 08:51:33 ON 08 MAY 2003

L6 0 S L1 AND BUTANEDIOL

FILE 'MEDLINE, CAPLUS, BIOSIS, AGRICOLA' ENTERED AT 08:52:04 ON 08 MAY 2003

L7 56 S L1 AND BUTANEDIOL  
L8 33 DUP REM L7 (23 DUPLICATES REMOVED)  
L9 0 S L8 AND D HIS

L10 ANSWER 6 OF 8 MEDLINE  
 AN 91024485 MEDLINE  
 DN 91024485 PubMed ID: 2222122  
 TI Purification and characterization of a (R)-2,3-  
**butanediol dehydrogenase** from *Saccharomyces cerevisiae*.  
 AU Heidlas J; Tressl R  
 CS Technische Universität Berlin, Fachbereich Lebensmitteltechnologie und  
 Biotechnologie.  
 SO ARCHIVES OF MICROBIOLOGY, (1990) 154 (3) 267-73.  
 Journal code: 0410427. ISSN: 0302-8933.  
 CY GERMANY: Germany, Federal Republic of  
 DT Journal; Article; (JOURNAL ARTICLE)  
 LA English  
 FS Priority Journals  
 EM 199011  
 ED Entered STN: 19910117  
 Last Updated on STN: 19970203  
 Entered Medline: 19901121  
 AB A NAD-dependent (R)-2,3-**butanediol**  
**dehydrogenase** (EC 1.1.1.4), selectively catalyzing the oxidation  
 at the (R)-center of 2,3-butanediol irrespective of the absolute  
 configuration of the other carbinol center, was isolated from cell  
 extracts of the yeast *Saccharomyces cerevisiae*. Purification was achieved  
 by means of streptomycin sulfate treatment, Sephadex G-25 filtration,  
 DEAE-Sephadex CL-6B chromatography, affinity chromatography on Matrex Gel  
 Blue A and Superose 6 prep grade chromatography leading to a 70-fold  
 enrichment of the specific activity with 44% yield. Analysis of chiral  
 products was carried out by gas chromatographic methods via  
 pre-chromatographic derivatization and resolution of corresponding  
 diastereomeric derivatives. The enzyme was capable to reduce irreversibly  
 diacetyl (2,3-butanediol) to (R)-acetoin (3-hydroxy-2-butanone) and in a  
 subsequent reaction reversibly to (R,R)-2,3-butanediol using NADH as  
 coenzyme. 1-Hydroxy-2-ketones and C5-acyloins were also accepted as  
 substrates, whereas the enzyme was inactive towards the reduction of  
 acetone and dihydroxyacetone. The relative molecular mass (Mr) of the  
 enzyme was estimated as 140,000 by means of gel filtration. On  
 SDS-polyacrylamide gel the protein decomposed into 4 (identical) subunits  
 of Mr 35,000. Optimum pH was 6.7 for the reduction of acetoin to  
 2,3-butanediol and 7.2 for the reverse reaction.